



SEQUENCE LISTING

<110> ROSIER, MARIE
PRADES, CATHERINE
ARNOULD, ISABELLE
DEAN, MICHAEL
ALLIKMETS, RANDO
DENEFLÉ, PATRICE

<120> NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS
CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF

<130> 03806.0534-00

<140> 10/090,280

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<210> 21
 <211> 198
 <212> DNA
 <213> Homo sapiens

<400> 21
 atgacctgtg ggccccagg caacaggacc atgtgtgagg tcggcgcggt gctggcagac 60
 atcggtcagc atgtgtacca gtgggtgtac actgcaagca tgggtttcat gctgggtgtt 120
 ggcgtcacca aaggcttcgt cttaccaag accacactga tggcatcctc ctctctgcat 180
 gacacggtgt ttgataag 198

<210> 22
 <211> 227
 <212> DNA
 <213> Homo sapiens

<400> 22
 atcttaaaga gccaatgag tttctttgac acgactccca ctggcaggct aatgaaccgt 60
 ttttccaagg atatggacga gctggatgtg aggcgtccgt ttcacgcaga gaactttctg 120
 cagcagtttt ttatgggtgt gtttattctc gtgatcttgg ctgctgtgtt tcctgctgtc 180
 ctttttagtcg tgccagcct tgctgtaggc ttcttcattc tgttacg 227

<210> 23
 <211> 138
 <212> DNA

<213> Homo sapiens

<400> 23

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cattttccac agaggagtcc aggagctcaa gaaggtggag aatgtcagcc ggtcaccctg 60
gttcacccac atcacctcct ccatgcaggg cctgggcatc attcacgcct atggcaagaa 120
ggagagctgc atcaccta                                     138
```

<210> 24

<211> 157

<212> DNA

<213> Homo sapiens

<400> 24

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tcacctcctc tactttaact gtgctctcag gtggtttgcg ctgagaatgg atgtcctcat 60
gaacatcctt accttcaact tggccttggt ggtgaccctg agtttctcct ccatcagtag 120
ttcatccaaa ggctgtgcat tgtcatacat catccag                                     157
```

<210> 25

<211> 90

<212> DNA

<213> Homo sapiens

<400> 25

```
ctgagcggac tgctccaagt gtgtgtgcga acgggaacag agacgcaagc caaattcacc 60
tccgtggagc tgctcaggga atacatttcg                                     90
```

<210> 26

<211> 190

<212> DNA

<213> Homo sapiens

<400> 26

```
acctgtgttc ctgaatgcac tcatcccctc aaagtgggga cctgtcccaa ggactggccc 60
agctgtgggg agatcacctt cagagactat cagatgagat acagagacaa cccccctt 120
gttctcgaca gcctgaactt gaacatacaa agtgggcaga cagtcgggat tgttggaaga 180
acaggttccg                                     190
```

<210> 27

<211> 160

<212> DNA

<213> Homo sapiens

<400> 27

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gaaagtcatc gttaggaatg gctttgtttc gtctgggtgga gccagccagt ggcacaatct 60
ttattgatga ggtggatata tgcatttctca gcttggaaga cctcagaacc aagctgactg 120
tgatcccaca ggatcctgtc ctgtttgtag gtacagtaag                                     160
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<210> 28

<211> 79

<212> DNA

<213> Homo sapiens

<400> 28
 gtacaacttg gatccctttg agagtcacac cgatgagatg ctctggcagg ttctggagag 60
 aacattcatg agagacaca 79

<210> 29
 <211> 114
 <212> DNA
 <213> Homo sapiens

<400> 29
 ataatgaaac tcccagaaaa attacaggca gaagtcacag aaaatggaga aaacttctca 60
 gtaggggaac gtcagctgct ttgtgtggcc cgagctcttc tccgtaattc aaag 114

<210> 30
 <211> 165
 <212> DNA
 <213> Homo sapiens

<400> 30
 atcattctcc ttgatgaagc caccgcctct atggactcca agactgacac cctgggttcag 60
 aacaccatca aagatgcctt caagggctgc actgtgctga ccatcgccca ccgcctcaac 120
 acagttctca actgcatca cgtcctgggt atggaaaatg ggaag 165

<210> 31
 <211> 289
 <212> DNA
 <213> Homo sapiens

<400> 31
 gtgattgagt ttgacaagcc tgaagtcctt gcagagaagc cagattctgc atttgcatg 60
 ttactagcag cagaagtcag attgtagagg tcctggcggc tgattctaga ggaggaagag 120
 gctctgtgag atgaatagga ggagtcttca ggaggagggg ctgtcctctc cgcaggcagc 180
 cctgggtcttc agccccctcc atccacggag tgagctgggg ctgaagttgt cccactgcc 240
 atactcagtc catgtcacc cacttggtgg gcttgggggt ggttctggg 289

<210> 32
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 32
 gatcctgaac acctttacaa tgcagcaatg gtggaagcct tcaaggagag ccctgctgag 60
 agagaggaag atgctggtat aatcg 85

<210> 33
 <211> 1356
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Val Gly Glu Gly Pro Tyr Leu Ile Ser Asp Leu Asp Gln Arg Gly
 1 5 10 15

Arg	Arg	Arg	Ser	Phe	Ala	Glu	Arg	Tyr	Asp	Pro	Ser	Leu	Lys	Thr	Met	20	25	30
Ile	Pro	Val	Arg	Pro	Cys	Ala	Arg	Leu	Ala	Pro	Asn	Pro	Val	Asp	Asp	35	40	45
Ala	Gly	Leu	Leu	Ser	Phe	Ala	Thr	Phe	Ser	Trp	Leu	Thr	Pro	Val	Met	50	55	60
Val	Lys	Gly	Tyr	Arg	Gln	Arg	Leu	Thr	Val	Asp	Thr	Leu	Pro	Pro	Leu	65	70	75
Ser	Thr	Tyr	Asp	Ser	Ser	Asp	Thr	Asn	Ala	Lys	Arg	Phe	Arg	Val	Leu	85	90	95
Trp	Asp	Glu	Glu	Val	Ala	Arg	Val	Gly	Pro	Glu	Lys	Ala	Ser	Leu	Ser	100	105	110
His	Val	Val	Trp	Lys	Phe	Gln	Arg	Thr	Arg	Val	Leu	Met	Asp	Ile	Val	115	120	125
Ala	Asn	Ile	Leu	Cys	Ile	Ile	Met	Ala	Ala	Ile	Gly	Pro	Thr	Val	Leu	130	135	140
Ile	His	Gln	Ile	Leu	Gln	Gln	Thr	Glu	Arg	Thr	Ser	Gly	Lys	Val	Trp	145	150	155
Val	Gly	Ile	Gly	Leu	Cys	Ile	Ala	Leu	Phe	Ala	Thr	Glu	Phe	Thr	Lys	165	170	175
Val	Phe	Phe	Trp	Ala	Leu	Ala	Trp	Ala	Ile	Asn	Tyr	Arg	Thr	Ala	Ile	180	185	190
Arg	Leu	Lys	Val	Ala	Leu	Ser	Thr	Leu	Val	Phe	Glu	Asn	Leu	Val	Ser	195	200	205
Phe	Lys	Thr	Leu	Thr	His	Ile	Ser	Val	Gly	Glu	Val	Leu	Asn	Ile	Leu	210	215	220
Ser	Ser	Asp	Ser	Tyr	Ser	Leu	Phe	Glu	Ala	Ala	Leu	Phe	Cys	Pro	Leu	225	230	235
Pro	Ala	Thr	Ile	Pro	Ile	Leu	Met	Val	Phe	Cys	Ala	Ala	Tyr	Ala	Phe	245	250	255
Phe	Ile	Leu	Gly	Pro	Thr	Ala	Leu	Ile	Gly	Ile	Ser	Val	Tyr	Val	Ile	260	265	270
Phe	Ile	Pro	Val	Gln	Met	Phe	Met	Ala	Lys	Leu	Asn	Ser	Ala	Phe	Arg	275	280	285
Arg	Ser	Ala	Ile	Leu	Val	Thr	Asp	Lys	Arg	Val	Gln	Thr	Met	Asn	Glu	290	295	300
Phe	Leu	Thr	Cys	Ile	Arg	Leu	Ile	Lys	Met	Tyr	Ala	Trp	Glu	Lys	Ser	305	310	315

Phe Thr Asn Thr Ile Gln Asp Ile Arg Arg Arg Glu Arg Lys Leu Leu
 325 330 335
 Glu Lys Ala Gly Phe Val Gln Ser Gly Asn Ser Ala Leu Ala Pro Ile
 340 345 350
 Val Ser Thr Ile Ala Ile Val Leu Thr Leu Ser Cys His Ile Leu Leu
 355 360 365
 Arg Arg Lys Leu Thr Ala Pro Val Ala Phe Ser Val Ile Ala Met Phe
 370 375 380
 Asn Val Met Lys Phe Ser Ile Ala Ile Leu Pro Phe Ser Ile Lys Ala
 385 390 395 400
 Met Ala Glu Ala Asn Val Ser Leu Arg Arg Met Lys Lys Ile Leu Ile
 405 410 415
 Asp Lys Ser Pro Pro Ser Tyr Ile Thr Gln Pro Glu Asp Pro Asp Thr
 420 425 430
 Val Leu Leu Leu Ala Asn Ala Thr Leu Thr Trp Glu His Glu Ala Ser
 435 440 445
 Arg Lys Ser Thr Pro Lys Lys Leu Gln Asn Gln Lys Arg His Leu Cys
 450 455 460
 Lys Lys Gln Arg Ser Glu Ala Tyr Ser Glu Arg Ser Pro Pro Ala Lys
 465 470 475 480
 Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp Ser Leu Lys Ser Val Leu
 485 490 495
 His Ser Ile Ser Phe Val Val Arg Lys Gly Lys Ile Leu Gly Ile Cys
 500 505 510
 Gly Asn Val Gly Ser Gly Lys Ser Ser Leu Leu Ala Ala Leu Leu Gly
 515 520 525
 Gln Met Gln Leu Gln Lys Gly Val Val Ala Val Asn Gly Thr Leu Ala
 530 535 540
 Tyr Val Ser Gln Gln Ala Trp Ile Phe His Gly Asn Val Arg Glu Asn
 545 550 555 560
 Ile Leu Phe Gly Glu Lys Tyr Asp His Gln Arg Tyr Gln His Thr Val
 565 570 575
 Arg Val Cys Gly Leu Gln Lys Asp Leu Ser Asn Leu Pro Tyr Gly Asp
 580 585 590
 Leu Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Arg
 595 600 605
 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Leu Tyr
 610 615 620

Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
 625 630 635 640
 Val Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
 645 650 655
 Leu Val Thr His Gln Leu Gln Phe Leu Glu Ser Cys Asp Glu Val Ile
 660 665 670
 Leu Leu Glu Asp Gly Glu Ile Cys Glu Lys Gly Thr His Lys Glu Leu
 675 680 685
 Met Glu Glu Arg Gly Arg Tyr Ala Lys Leu Ile His Asn Leu Arg Gly
 690 695 700
 Leu Gln Phe Lys Asp Pro Glu His Leu Tyr Asn Ala Ala Met Val Glu
 705 710 715 720
 Ala Phe Lys Glu Ser Pro Ala Glu Arg Glu Glu Asp Ala Val Leu Ala
 725 730 735
 Pro Gly Asn Glu Lys Asp Glu Gly Lys Glu Ser Glu Thr Gly Ser Glu
 740 745 750
 Phe Val Asp Thr Lys Val Pro Glu His Gln Leu Ile Gln Thr Glu Ser
 755 760 765
 Pro Gln Glu Gly Thr Val Thr Trp Lys Thr Tyr His Thr Tyr Ile Lys
 770 775 780
 Ala Ser Gly Gly Tyr Leu Leu Ser Leu Phe Thr Val Phe Leu Phe Leu
 785 790 795 800
 Leu Met Ile Gly Ser Ala Ala Phe Ser Asn Trp Trp Leu Gly Leu Trp
 805 810 815
 Leu Asp Lys Gly Ser Arg Met Thr Cys Gly Pro Gln Gly Asn Arg Thr
 820 825 830
 Met Cys Glu Val Gly Ala Val Leu Ala Asp Ile Gly Gln His Val Tyr
 835 840 845
 Gln Trp Val Tyr Thr Ala Ser Met Val Phe Met Leu Val Phe Gly Val
 850 855 860
 Thr Lys Gly Phe Val Phe Thr Lys Thr Thr Leu Met Ala Ser Ser Ser
 865 870 875 880
 Leu His Asp Thr Val Phe Asp Lys Ile Leu Lys Ser Pro Met Ser Phe
 885 890 895
 Phe Asp Thr Thr Pro Thr Gly Arg Leu Met Asn Arg Phe Ser Lys Asp
 900 905 910
 Met Asp Glu Leu Asp Val Arg Leu Pro Phe His Ala Glu Asn Phe Leu
 915 920 925

Gln Gln Phe Phe Met Val Val Phe Ile Leu Val Ile Leu Ala Ala Val
 930 935 940
 Phe Pro Ala Val Leu Leu Val Val Ala Ser Leu Ala Val Gly Phe Phe
 945 950 955 960
 Ile Leu Leu Arg Ile Phe His Arg Gly Val Gln Glu Leu Lys Lys Val
 965 970 975
 Glu Asn Val Ser Arg Ser Pro Trp Phe Thr His Ile Thr Ser Ser Met
 980 985 990
 Gln Gly Leu Gly Ile Ile His Ala Tyr Gly Lys Lys Glu Ser Cys Ile
 995 1000 1005
 Thr Tyr His Leu Leu Tyr Phe Asn Cys Ala Leu Arg Trp Phe Ala Leu
 1010 1015 1020
 Arg Met Asp Val Leu Met Asn Ile Leu Thr Phe Thr Val Ala Leu Leu
 1025 1030 1035 1040
 Val Thr Leu Ser Phe Ser Ser Ile Ser Thr Ser Ser Lys Gly Leu Ser
 1045 1050 1055
 Leu Ser Tyr Ile Ile Gln Leu Ser Gly Leu Leu Gln Val Cys Val Arg
 1060 1065 1070
 Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu Leu Leu Arg
 1075 1080 1085
 Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro Leu Lys Val
 1090 1095 1100
 Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile Thr Phe Arg
 1105 1110 1115 1120
 Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val Leu Asp Ser
 1125 1130 1135
 Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile Val Gly Arg
 1140 1145 1150
 Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val
 1155 1160 1165
 Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp Ile Cys Ile
 1170 1175 1180
 Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile Pro Gln Asp
 1185 1190 1195 1200
 Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp Pro Phe Glu
 1205 1210 1215
 Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg Thr Phe Met
 1220 1225 1230

Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala Glu Val Thr
 1235 1240 1245
 Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Val
 1250 1255 1260
 Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu Asp Glu Ala
 1265 1270 1275 1280
 Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln Asn Thr Ile
 1285 1290 1295
 Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala His Arg Leu
 1300 1305 1310
 Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu Asn Gly Lys
 1315 1320 1325
 Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys Pro Asp Ser
 1330 1335 1340
 Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu
 1345 1350 1355

<210> 34
 <211> 1359
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Val Gly Glu Gly Pro Tyr Leu Ile Ser Asp Leu Asp Gln Arg Gly
 1 5 10 15
 Arg Arg Arg Ser Phe Ala Glu Arg Tyr Asp Pro Ser Leu Lys Thr Met
 20 25 30
 Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp
 35 40 45
 Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met
 50 55 60
 Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu
 65 70 75 80
 Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu
 85 90 95
 Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser
 100 105 110
 His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val
 115 120 125
 Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu
 130 135 140

Ile	His	Gln	Ile	Leu	Gln	Gln	Thr	Glu	Arg	Thr	Ser	Gly	Lys	Val	Trp	145	150	155	160
Val	Gly	Ile	Gly	Leu	Cys	Ile	Ala	Leu	Phe	Ala	Thr	Glu	Phe	Thr	Lys	165	170	175	
Val	Phe	Phe	Trp	Ala	Leu	Ala	Trp	Ala	Ile	Asn	Tyr	Arg	Thr	Ala	Ile	180	185	190	
Arg	Leu	Lys	Val	Ala	Leu	Ser	Thr	Leu	Val	Phe	Glu	Asn	Leu	Val	Ser	195	200	205	
Phe	Lys	Thr	Leu	Thr	His	Ile	Ser	Val	Gly	Glu	Val	Leu	Asn	Ile	Leu	210	215	220	
Ser	Ser	Asp	Ser	Tyr	Ser	Leu	Phe	Glu	Ala	Ala	Leu	Phe	Cys	Pro	Leu	225	230	235	240
Pro	Ala	Thr	Ile	Pro	Ile	Leu	Met	Val	Phe	Cys	Ala	Ala	Tyr	Ala	Phe	245	250	255	
Phe	Ile	Leu	Gly	Pro	Thr	Ala	Leu	Ile	Gly	Ile	Ser	Val	Tyr	Val	Ile	260	265	270	
Phe	Ile	Pro	Val	Gln	Met	Phe	Met	Ala	Lys	Leu	Asn	Ser	Ala	Phe	Arg	275	280	285	
Arg	Ser	Ala	Ile	Leu	Val	Thr	Asp	Lys	Arg	Val	Gln	Thr	Met	Asn	Glu	290	295	300	
Phe	Leu	Thr	Cys	Ile	Arg	Leu	Ile	Lys	Met	Tyr	Ala	Trp	Glu	Lys	Ser	305	310	315	320
Phe	Thr	Asn	Thr	Ile	Gln	Asp	Ile	Arg	Arg	Arg	Glu	Arg	Lys	Leu	Leu	325	330	335	
Glu	Lys	Ala	Gly	Phe	Val	Gln	Ser	Gly	Asn	Ser	Ala	Leu	Ala	Pro	Ile	340	345	350	
Val	Ser	Thr	Ile	Ala	Ile	Val	Leu	Thr	Leu	Ser	Cys	His	Ile	Leu	Leu	355	360	365	
Arg	Arg	Lys	Leu	Thr	Ala	Pro	Val	Ala	Phe	Ser	Val	Ile	Ala	Met	Phe	370	375	380	
Asn	Val	Met	Lys	Phe	Ser	Ile	Ala	Ile	Leu	Pro	Phe	Ser	Ile	Lys	Ala	385	390	395	400
Met	Ala	Glu	Ala	Asn	Val	Ser	Leu	Arg	Arg	Met	Lys	Lys	Ile	Leu	Ile	405	410	415	
Asp	Lys	Ser	Pro	Pro	Ser	Tyr	Ile	Thr	Gln	Pro	Glu	Asp	Pro	Asp	Thr	420	425	430	
Val	Leu	Leu	Leu	Ala	Asn	Ala	Thr	Leu	Thr	Trp	Glu	His	Glu	Ala	Ser	435	440	445	

Arg Lys Ser Thr Pro Lys Lys Leu Gln Asn Gln Lys Arg His Leu Cys
 450 455 460
 Lys Lys Gln Arg Ser Glu Ala Tyr Ser Glu Arg Ser Pro Pro Ala Lys
 465 470 475 480
 Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp Ser Leu Lys Ser Val Leu
 485 490 495
 His Ser Ile Ser Phe Val Val Arg Lys Gly Lys Ile Leu Gly Ile Cys
 500 505 510
 Gly Asn Val Gly Ser Gly Lys Ser Ser Leu Leu Ala Ala Leu Leu Gly
 515 520 525
 Gln Met Gln Leu Gln Lys Gly Val Val Ala Val Asn Gly Thr Leu Ala
 530 535 540
 Tyr Val Ser Gln Gln Ala Trp Ile Phe His Gly Asn Val Arg Glu Asn
 545 550 555 560
 Ile Leu Phe Gly Glu Lys Tyr Asp His Gln Arg Tyr Gln His Thr Val
 565 570 575
 Arg Val Cys Gly Leu Gln Lys Asp Leu Ser Asn Leu Pro Tyr Gly Asp
 580 585 590
 Leu Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Arg
 595 600 605
 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Leu Tyr
 610 615 620
 Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
 625 630 635 640
 Val Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
 645 650 655
 Leu Val Thr His Gln Leu Gln Phe Leu Glu Ser Cys Asp Glu Val Ile
 660 665 670
 Leu Leu Glu Asp Gly Glu Ile Cys Glu Lys Gly Thr His Lys Glu Leu
 675 680 685
 Met Glu Glu Arg Gly Arg Tyr Ala Lys Leu Ile His Asn Leu Arg Gly
 690 695 700
 Leu Gln Phe Lys Asp Pro Glu His Leu Tyr Asn Ala Ala Met Val Glu
 705 710 715 720
 Ala Phe Lys Glu Ser Pro Ala Glu Arg Glu Glu Asp Ala Gly Ile Ile
 725 730 735
 Val Leu Ala Pro Gly Asn Glu Lys Asp Glu Gly Lys Glu Ser Glu Thr
 740 745 750

Gly Ser Glu Phe Val Asp Thr Lys Val Pro Glu His Gln Leu Ile Gln
 755 760 765
 Thr Glu Ser Pro Gln Glu Gly Thr Val Thr Trp Lys Thr Tyr His Thr
 770 775 780
 Tyr Ile Lys Ala Ser Gly Gly Tyr Leu Leu Ser Leu Phe Thr Val Phe
 785 790 795 800
 Leu Phe Leu Leu Met Ile Gly Ser Ala Ala Phe Ser Asn Trp Trp Leu
 805 810 815
 Gly Leu Trp Leu Asp Lys Gly Ser Arg Met Thr Cys Gly Pro Gln Gly
 820 825 830
 Asn Arg Thr Met Cys Glu Val Gly Ala Val Leu Ala Asp Ile Gly Gln
 835 840 845
 His Val Tyr Gln Trp Val Tyr Thr Ala Ser Met Val Phe Met Leu Val
 850 855 860
 Phe Gly Val Thr Lys Gly Phe Val Phe Thr Lys Thr Thr Leu Met Ala
 865 870 875 880
 Ser Ser Ser Leu His Asp Thr Val Phe Asp Lys Ile Leu Lys Ser Pro
 885 890 895
 Met Ser Phe Phe Asp Thr Thr Pro Thr Gly Arg Leu Met Asn Arg Phe
 900 905 910
 Ser Lys Asp Met Asp Glu Leu Asp Val Arg Leu Pro Phe His Ala Glu
 915 920 925
 Asn Phe Leu Gln Gln Phe Phe Met Val Val Phe Ile Leu Val Ile Leu
 930 935 940
 Ala Ala Val Phe Pro Ala Val Leu Leu Val Val Ala Ser Leu Ala Val
 945 950 955 960
 Gly Phe Phe Ile Leu Leu Arg Ile Phe His Arg Gly Val Gln Glu Leu
 965 970 975
 Lys Lys Val Glu Asn Val Ser Arg Ser Pro Trp Phe Thr His Ile Thr
 980 985 990
 Ser Ser Met Gln Gly Leu Gly Ile Ile His Ala Tyr Gly Lys Lys Glu
 995 1000 1005
 Ser Cys Ile Thr Tyr His Leu Leu Tyr Phe Asn Cys Ala Leu Arg Trp
 1010 1015 1020
 Phe Ala Leu Arg Met Asp Val Leu Met Asn Ile Leu Thr Phe Thr Val
 1025 1030 1035 1040
 Ala Leu Leu Val Thr Leu Ser Phe Ser Ser Ile Ser Thr Ser Ser Lys
 1045 1050 1055

Gly Leu Ser Leu Ser Tyr Ile Ile Gln Leu Ser Gly Leu Leu Gln Val
 1060 1065 1070
 Cys Val Arg Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu
 1075 1080 1085
 Leu Leu Arg Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro
 1090 1095 1100
 Leu Lys Val Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile
 1105 1110 1115 1120
 Thr Phe Arg Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val
 1125 1130 1135
 Leu Asp Ser Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile
 1140 1145 1150
 Val Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe
 1155 1160 1165
 Arg Leu Val Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp
 1170 1175 1180
 Ile Cys Ile Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile
 1185 1190 1195 1200
 Pro Gln Asp Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp
 1205 1210 1215
 Pro Phe Glu Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg
 1220 1225 1230
 Thr Phe Met Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala
 1235 1240 1245
 Glu Val Thr Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu
 1250 1255 1260
 Leu Cys Val Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu
 1265 1270 1275 1280
 Asp Glu Ala Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln
 1285 1290 1295
 Asn Thr Ile Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala
 1300 1305 1310
 His Arg Leu Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu
 1315 1320 1325
 Asn Gly Lys Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys
 1330 1335 1340
 Pro Asp Ser Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu
 1345 1350 1355

<210> 35
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 35
 tccttcgcca cattttcc

18

<210> 36
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 36
 attgagcacc tcgccaac

18

<210> 37
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 37
 ttctcattca ccaaatactc c

21

<210> 38
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 38
 acattaaaca tggcaatcac ac

22

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Synthetic primer

<400> 39

gtgtgattgc catgtttaat gt

22

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Synthetic primer

<400> 40

ggagtgcatt aagaagacgc

20

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Synthetic primer

<400> 41

cagagaggag gatgccat

18

<210> 42

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Synthetic primer

<400> 42

cactgcaagc atggtgttc

19

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Synthetic primer

<400> 43

ctcatcggtg tgactctca

19

<210> 44
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 44
 tttgagagtc acaccgatga gat 23

<210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 45
 cccagaacca accccaag 18

<210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the Artificial Sequence: Synthetic
 primer

<400> 46
 ggctctgtga gatgaatagg 20

<210> 47
 <211> 1376
 <212> PRT
 <213> Homo sapiens

<400> 47
 Met Thr Arg Lys Arg Thr Tyr Trp Val Pro Asn Ser Ser Gly Gly Leu
 1 5 10 15

Val Asn Arg Gly Ile Asp Ile Gly Asp Asp Met Val Ser Gly Leu Ile
 20 25 30

Tyr Lys Thr Tyr Thr Leu Gln Asp Gly Pro Trp Ser Gln Gln Glu Arg
 35 40 45

Asn Pro Glu Ala Pro Gly Arg Ala Ala Val Pro Pro Trp Gly Lys Tyr
 50 55 60

Asp	Ala	Ala	Leu	Arg	Thr	Met	Ile	Pro	Phe	Arg	Pro	Lys	Pro	Arg	Phe	65	70	75	80
Pro	Ala	Pro	Gln	Pro	Leu	Asp	Asn	Ala	Gly	Leu	Phe	Ser	Tyr	Leu	Thr	85	90	95	
Val	Ser	Trp	Leu	Thr	Pro	Leu	Met	Ile	Gln	Ser	Leu	Arg	Ser	Arg	Leu	100	105	110	
Asp	Glu	Asn	Thr	Ile	Pro	Pro	Leu	Ser	Val	His	Asp	Ala	Ser	Asp	Lys	115	120	125	
Asn	Val	Gln	Arg	Leu	His	Arg	Leu	Trp	Glu	Glu	Glu	Val	Ser	Arg	Arg	130	135	140	
Gly	Ile	Glu	Lys	Ala	Ser	Val	Leu	Leu	Val	Met	Leu	Arg	Phe	Gln	Arg	145	150	155	160
Thr	Arg	Leu	Ile	Phe	Asp	Ala	Leu	Leu	Gly	Ile	Cys	Phe	Cys	Ile	Ala	165	170	175	
Ser	Val	Leu	Gly	Pro	Ile	Leu	Ile	Ile	Pro	Lys	Ile	Leu	Glu	Tyr	Ser	180	185	190	
Glu	Glu	Gln	Leu	Gly	Asn	Val	Val	His	Gly	Val	Gly	Leu	Cys	Phe	Ala	195	200	205	
Leu	Phe	Leu	Ser	Glu	Cys	Val	Lys	Ser	Leu	Ser	Phe	Ser	Ser	Ser	Trp	210	215	220	
Ile	Ile	Asn	Gln	Arg	Thr	Ala	Ile	Arg	Phe	Arg	Ala	Ala	Val	Ser	Ser	225	230	235	240
Phe	Ala	Phe	Glu	Lys	Leu	Ile	Gln	Phe	Lys	Ser	Val	Ile	His	Ile	Thr	245	250	255	
Ser	Gly	Glu	Ala	Ile	Ser	Phe	Phe	Thr	Gly	Asp	Val	Asn	Tyr	Leu	Phe	260	265	270	
Glu	Gly	Val	Cys	Tyr	Gly	Pro	Leu	Val	Leu	Ile	Thr	Cys	Ala	Ser	Leu	275	280	285	
Val	Ile	Cys	Ser	Ile	Ser	Ser	Tyr	Phe	Ile	Ile	Gly	Tyr	Thr	Ala	Phe	290	295	300	
Ile	Ala	Ile	Leu	Cys	Tyr	Leu	Leu	Val	Phe	Pro	Leu	Ala	Val	Phe	Met	305	310	315	320
Thr	Arg	Met	Ala	Val	Lys	Ala	Gln	His	His	Thr	Ser	Glu	Val	Ser	Asp	325	330	335	
Gln	Arg	Ile	Arg	Val	Thr	Ser	Glu	Val	Leu	Thr	Cys	Ile	Lys	Leu	Ile	340	345	350	
Lys	Met	Tyr	Thr	Trp	Glu	Lys	Pro	Phe	Ala	Lys	Ile	Ile	Glu	Asp	Leu	355	360	365	

Arg	Arg	Lys	Glu	Arg	Lys	Leu	Leu	Glu	Lys	Cys	Gly	Leu	Val	Gln	Ser		
370						375					380						
Leu	Thr	Ser	Ile	Thr	Leu	Phe	Ile	Ile	Pro	Thr	Val	Ala	Thr	Ala	Val		
385					390				395						400		
Trp	Val	Leu	Ile	His	Thr	Ser	Leu	Lys	Leu	Lys	Leu	Thr	Ala	Ser	Met		
				405				410						415			
Ala	Phe	Ser	Met	Leu	Ala	Ser	Leu	Asn	Leu	Leu	Arg	Leu	Ser	Val	Phe		
			420					425					430				
Phe	Val	Pro	Ile	Ala	Val	Lys	Gly	Leu	Thr	Asn	Ser	Lys	Ser	Ala	Val		
		435					440					445					
Met	Arg	Phe	Lys	Lys	Phe	Phe	Leu	Gln	Glu	Ser	Pro	Val	Phe	Tyr	Val		
	450					455					460						
Gln	Thr	Leu	Gln	Asp	Pro	Ser	Lys	Ala	Leu	Val	Phe	Glu	Glu	Ala	Thr		
465					470					475					480		
Leu	Ser	Trp	Gln	Gln	Thr	Cys	Pro	Gly	Ile	Val	Asn	Gly	Ala	Leu	Glu		
			485					490						495			
Leu	Glu	Arg	Asn	Gly	His	Ala	Ser	Glu	Gly	Met	Thr	Arg	Pro	Arg	Asp		
			500					505					510				
Ala	Leu	Gly	Pro	Glu	Glu	Glu	Gly	Asn	Ser	Leu	Gly	Pro	Glu	Leu	His		
		515					520					525					
Lys	Ile	Asn	Leu	Val	Val	Ser	Lys	Gly	Met	Met	Leu	Gly	Val	Cys	Gly		
	530					535					540						
Asn	Thr	Gly	Ser	Gly	Lys	Ser	Ser	Leu	Leu	Ser	Ala	Ile	Leu	Glu	Glu		
545					550					555					560		
Met	His	Leu	Leu	Glu	Gly	Ser	Val	Gly	Val	Gln	Gly	Ser	Leu	Ala	Tyr		
				565				570						575			
Val	Pro	Gln	Gln	Ala	Trp	Ile	Val	Ser	Gly	Asn	Ile	Arg	Glu	Asn	Ile		
			580					585					590				
Leu	Met	Gly	Gly	Ala	Tyr	Asp	Lys	Ala	Arg	Thr	Pro	Gly	Cys	Ala	Cys		
	595					600						605					
Cys	Leu	Asp	Met	Val	Pro	Phe	Thr	Ala	Cys	Leu	Gln	Ile	Gly	Glu	Arg		
	610					615					620						
Gly	Leu	Asn	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Ile	Ser	Leu	Ala	Arg		
625					630					635					640		
Ala	Val	Tyr	Ser	Asp	Arg	Gln	Ile	Tyr	Leu	Leu	Asp	Asp	Pro	Leu	Ser		
				645					650					655			
Ala	Val	Asp	Ala	His	Val	Gly	Lys	His	Ile	Phe	Glu	Glu	Cys	Ile	Lys		
			660					665					670				

Lys	Thr	Leu	Arg	Gly	Lys	Thr	Val	Val	Leu	Val	Thr	His	Gln	Leu	Gln	
		675					680					685				
Tyr	Leu	Glu	Phe	Cys	Gly	Gln	Ile	Ile	Leu	Leu	Glu	Asn	Gly	Lys	Ile	
	690					695					700					
Cys	Glu	Asn	Gly	Thr	His	Ser	Glu	Leu	Met	Gln	Lys	Lys	Gly	Lys	Tyr	
705					710					715					720	
Ala	Gln	Leu	Ile	Gln	Lys	Met	His	Lys	Glu	Ala	Thr	Ser	Asp	Met	Leu	
				725					730					735		
Gln	Asp	Thr	Ala	Lys	Ile	Ala	Glu	Lys	Pro	Lys	Val	Glu	Ser	Gln	Ala	
			740					745						750		
Leu	Ala	Thr	Ser	Leu	Glu	Glu	Ser	Leu	Asn	Gly	Asn	Ala	Val	Pro	Glu	
		755					760					765				
His	Gln	Leu	Thr	Gln	Glu	Glu	Glu	Met	Glu	Glu	Gly	Ser	Leu	Ser	Trp	
	770					775					780					
Arg	Val	Tyr	His	His	Tyr	Ile	Gln	Ala	Ala	Gly	Gly	Tyr	Met	Val	Ser	
785					790					795					800	
Cys	Ile	Ile	Phe	Phe	Phe	Val	Val	Leu	Ile	Val	Phe	Leu	Thr	Ile	Phe	
			805						810					815		
Ser	Phe	Trp	Trp	Leu	Ser	Tyr	Trp	Leu	Glu	Gln	Gly	Ser	Gly	Thr	Asn	
			820					825					830			
Ser	Ser	Arg	Glu	Ser	Asn	Gly	Thr	Met	Ala	Asp	Leu	Gly	Asn	Ile	Ala	
		835					840					845				
Asp	Asn	Pro	Gln	Leu	Ser	Phe	Tyr	Gln	Leu	Val	Tyr	Gly	Leu	Asn	Ala	
	850					855					860					
Leu	Leu	Leu	Ile	Cys	Val	Gly	Val	Cys	Ser	Ser	Gly	Ile	Phe	Thr	Lys	
865				870						875					880	
Val	Thr	Arg	Lys	Ala	Ser	Thr	Ala	Leu	His	Asn	Lys	Leu	Phe	Asn	Lys	
				885					890					895		
Val	Phe	Arg	Cys	Pro	Met	Ser	Phe	Phe	Asp	Thr	Ile	Pro	Ile	Gly	Arg	
			900					905					910			
Leu	Leu	Asn	Cys	Phe	Ala	Gly	Asp	Leu	Glu	Gln	Leu	Asp	Gln	Leu	Leu	
		915					920					925				
Pro	Ile	Phe	Ser	Glu	Gln	Phe	Leu	Val	Leu	Ser	Leu	Met	Val	Ile	Ala	
	930					935					940					
Val	Leu	Leu	Ile	Val	Ser	Val	Leu	Ser	Pro	Tyr	Ile	Leu	Leu	Met	Gly	
945					950					955					960	
Ala	Ile	Ile	Met	Val	Ile	Cys	Phe	Ile	Tyr	Tyr	Met	Met	Phe	Lys	Lys	
				965					970					975		

Ala Ile Gly Val Phe Lys Arg Leu Glu Asn Tyr Ser Arg Ser Pro Leu
 980 985 990
 Phe Ser His Ile Leu Asn Ser Leu Gln Gly Leu Ser Ser Ile His Val
 995 1000 1005
 Tyr Gly Lys Thr Glu Asp Phe Ile Ser Gln Phe Lys Arg Leu Thr Asp
 1010 1015 1020
 Ala Gln Asn Asn Tyr Leu Leu Leu Phe Leu Ser Ser Thr Arg Trp Met
 1025 1030 1035 1040
 Ala Leu Arg Leu Glu Ile Met Thr Asn Leu Val Thr Leu Ala Val Ala
 1045 1050 1055
 Leu Phe Val Ala Phe Gly Ile Ser Ser Thr Pro Tyr Ser Phe Lys Val
 1060 1065 1070
 Met Ala Val Asn Ile Val Leu Gln Leu Ala Ser Ser Phe Gln Ala Thr
 1075 1080 1085
 Ala Arg Ile Gly Leu Glu Thr Glu Ala Gln Phe Thr Ala Val Glu Arg
 1090 1095 1100
 Ile Leu Gln Tyr Met Lys Met Cys Val Ser Glu Ala Pro Leu His Met
 1105 1110 1115 1120
 Glu Gly Thr Ser Cys Pro Gln Gly Trp Pro Gln His Gly Glu Ile Ile
 1125 1130 1135
 Phe Gln Asp Tyr His Met Lys Tyr Arg Asp Asn Thr Pro Thr Val Leu
 1140 1145 1150
 His Gly Ile Asn Leu Thr Ile Arg Gly His Glu Val Val Gly Ile Val
 1155 1160 1165
 Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe Arg
 1170 1175 1180
 Leu Val Glu Pro Met Ala Gly Arg Ile Leu Ile Asp Gly Val Asp Ile
 1185 1190 1195 1200
 Cys Ser Ile Gly Leu Glu Asp Leu Arg Ser Lys Leu Ser Val Ile Pro
 1205 1210 1215
 Gln Asp Pro Val Leu Leu Ser Gly Thr Ile Arg Phe Asn Leu Asp Pro
 1220 1225 1230
 Phe Asp Arg His Thr Asp Gln Gln Ile Trp Asp Ala Leu Glu Arg Thr
 1235 1240 1245
 Phe Leu Thr Lys Ala Ile Ser Lys Phe Pro Lys Lys Leu His Thr Asp
 1250 1255 1260
 Val Val Glu Asn Gly Gly Asn Phe Ser Val Gly Glu Arg Gln Leu Leu
 1265 1270 1275 1280

Cys Ile Ala Arg Ala Val Leu Arg Asn Ser Lys Ile Ile Leu Ile Asp
 1285 1290 1295
 Glu Ala Thr Ala Ser Ile Asp Met Glu Thr Asp Thr Leu Ile Gln Arg
 1300 1305 1310
 Thr Ile Arg Glu Ala Phe Gln Gly Cys Thr Val Leu Val Ile Ala His
 1315 1320 1325
 Arg Val Thr Thr Val Leu Asn Cys Asp His Ile Leu Val Met Gly Asn
 1330 1335 1340
 Gly Lys Val Val Glu Phe Asp Arg Pro Glu Val Leu Arg Lys Lys Pro
 1345 1350 1355 1360
 Gly Ser Leu Phe Ala Ala Leu Met Ala Thr Ala Thr Ser Ser Leu Arg
 1365 1370 1375

<210> 48
 <211> 1437
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Lys Asp Ile Asp Ile Gly Lys Glu Tyr Ile Ile Pro Ser Pro Gly
 1 5 10 15
 Tyr Arg Ser Val Arg Glu Arg Thr Ser Thr Ser Gly Thr His Arg Asp
 20 25 30
 Arg Glu Asp Ser Lys Phe Arg Arg Thr Arg Pro Leu Glu Cys Gln Asp
 35 40 45
 Ala Leu Glu Thr Ala Ala Arg Ala Glu Gly Leu Ser Leu Asp Ala Ser
 50 55 60
 Met His Ser Gln Leu Arg Ile Leu Asp Glu Glu His Pro Lys Gly Lys
 65 70 75 80
 Tyr His His Gly Leu Ser Ala Leu Lys Pro Ile Arg Thr Thr Ser Lys
 85 90 95
 His Gln His Pro Val Asp Asn Ala Gly Leu Phe Ser Cys Met Thr Phe
 100 105 110
 Ser Trp Leu Ser Ser Leu Ala Arg Val Ala His Lys Lys Gly Glu Leu
 115 120 125
 Ser Met Glu Asp Val Trp Ser Leu Ser Lys His Glu Ser Ser Asp Val
 130 135 140
 Asn Cys Arg Arg Leu Glu Arg Leu Trp Gln Glu Glu Leu Asn Glu Val
 145 150 155 160
 Gly Pro Asp Ala Ala Ser Leu Arg Arg Val Val Trp Ile Phe Cys Arg
 165 170 175

Thr	Arg	Leu	Ile	Leu	Ser	Ile	Val	Cys	Leu	Met	Ile	Thr	Gln	Leu	Ala	180	185	190
Gly	Phe	Ser	Gly	Pro	Ala	Phe	Met	Val	Lys	His	Leu	Leu	Glu	Tyr	Thr	195	200	205
Gln	Ala	Thr	Glu	Ser	Asn	Leu	Gln	Tyr	Ser	Leu	Leu	Leu	Val	Leu	Gly	210	215	220
Leu	Leu	Leu	Thr	Glu	Ile	Val	Arg	Ser	Trp	Ser	Leu	Ala	Leu	Thr	Trp	225	230	235
Ala	Leu	Asn	Tyr	Arg	Thr	Gly	Val	Arg	Leu	Arg	Gly	Ala	Ile	Leu	Thr	245	250	255
Met	Ala	Phe	Lys	Lys	Ile	Leu	Lys	Leu	Lys	Asn	Ile	Lys	Glu	Lys	Ser	260	265	270
Leu	Gly	Glu	Leu	Ile	Asn	Ile	Cys	Ser	Asn	Asp	Gly	Gln	Arg	Met	Phe	275	280	285
Glu	Ala	Ala	Ala	Val	Gly	Ser	Leu	Leu	Ala	Gly	Gly	Pro	Val	Val	Ala	290	295	300
Ile	Leu	Gly	Met	Ile	Tyr	Asn	Val	Ile	Ile	Leu	Gly	Pro	Thr	Gly	Phe	305	310	315
Leu	Gly	Ser	Ala	Val	Phe	Ile	Leu	Phe	Tyr	Pro	Ala	Met	Met	Phe	Ala	325	330	335
Ser	Arg	Leu	Thr	Ala	Tyr	Phe	Arg	Arg	Lys	Cys	Val	Ala	Ala	Thr	Asp	340	345	350
Glu	Arg	Val	Gln	Lys	Met	Asn	Glu	Val	Leu	Thr	Tyr	Ile	Lys	Phe	Ile	355	360	365
Lys	Met	Tyr	Ala	Trp	Val	Lys	Ala	Phe	Ser	Gln	Ser	Val	Gln	Lys	Ile	370	375	380
Arg	Glu	Glu	Glu	Arg	Arg	Ile	Leu	Glu	Lys	Ala	Gly	Tyr	Phe	Gln	Gly	385	390	395
Ile	Thr	Val	Gly	Val	Ala	Pro	Ile	Val	Val	Val	Ile	Ala	Ser	Val	Val	405	410	415
Thr	Phe	Ser	Val	His	Met	Thr	Leu	Gly	Phe	Asp	Leu	Thr	Ala	Ala	Gln	420	425	430
Ala	Phe	Thr	Val	Val	Thr	Val	Phe	Asn	Ser	Met	Thr	Phe	Ala	Leu	Lys	435	440	445
Val	Thr	Pro	Phe	Ser	Val	Lys	Ser	Leu	Ser	Glu	Ala	Ser	Val	Ala	Val	450	455	460
Asp	Arg	Phe	Lys	Ser	Leu	Phe	Leu	Met	Glu	Glu	Val	His	Met	Ile	Lys	465	470	475

Asn	Lys	Pro	Ala	Ser	Pro	His	Ile	Lys	Ile	Glu	Met	Lys	Asn	Ala	Thr	485	490	495
Leu	Ala	Trp	Asp	Ser	Ser	His	Ser	Ser	Ile	Gln	Asn	Ser	Pro	Lys	Leu	500	505	510
Thr	Pro	Lys	Met	Lys	Lys	Asp	Lys	Arg	Ala	Ser	Arg	Gly	Lys	Lys	Glu	515	520	525
Lys	Val	Arg	Gln	Leu	Gln	Arg	Thr	Glu	His	Gln	Ala	Val	Leu	Ala	Glu	530	535	540
Gln	Lys	Gly	His	Leu	Leu	Leu	Asp	Ser	Asp	Glu	Arg	Pro	Ser	Pro	Glu	545	550	555
Glu	Glu	Glu	Gly	Lys	His	Ile	His	Leu	Gly	His	Leu	Arg	Leu	Gln	Arg	565	570	575
Thr	Leu	His	Ser	Ile	Asp	Leu	Glu	Ile	Gln	Glu	Gly	Lys	Leu	Val	Gly	580	585	590
Ile	Cys	Gly	Ser	Val	Gly	Ser	Gly	Lys	Thr	Ser	Leu	Ile	Ser	Ala	Ile	595	600	605
Leu	Gly	Gln	Met	Thr	Leu	Leu	Glu	Gly	Ser	Ile	Ala	Ile	Ser	Gly	Thr	610	615	620
Phe	Ala	Tyr	Val	Ala	Gln	Gln	Ala	Trp	Ile	Leu	Asn	Ala	Thr	Leu	Arg	625	630	635
Asp	Asn	Ile	Leu	Phe	Gly	Lys	Glu	Tyr	Asp	Glu	Glu	Arg	Tyr	Asn	Ser	645	650	655
Val	Leu	Asn	Ser	Cys	Cys	Leu	Arg	Pro	Asp	Leu	Ala	Ile	Leu	Pro	Ser	660	665	670
Ser	Asp	Leu	Thr	Glu	Ile	Gly	Glu	Arg	Gly	Ala	Asn	Leu	Ser	Gly	Gly	675	680	685
Gln	Arg	Gln	Arg	Ile	Ser	Leu	Ala	Arg	Ala	Leu	Tyr	Ser	Asp	Arg	Ser	690	695	700
Ile	Tyr	Ile	Leu	Asp	Asp	Pro	Leu	Ser	Ala	Leu	Asp	Ala	His	Val	Gly	705	710	715
Asn	His	Ile	Phe	Asn	Ser	Ala	Ile	Arg	Lys	His	Leu	Lys	Ser	Lys	Thr	725	730	735
Val	Leu	Phe	Val	Thr	His	Gln	Leu	Gln	Tyr	Leu	Val	Asp	Cys	Asp	Glu	740	745	750
Val	Ile	Phe	Met	Lys	Glu	Gly	Cys	Ile	Thr	Glu	Arg	Gly	Thr	His	Glu	755	760	765
Glu	Leu	Met	Asn	Leu	Asn	Gly	Asp	Tyr	Ala	Thr	Ile	Phe	Asn	Asn	Leu	770	775	780

Leu Leu Gly Glu Thr Pro Pro Val Glu Ile Asn Ser Lys Lys Glu Thr
 785 790 795 800
 Ser Gly Ser Gln Lys Lys Ser Gln Asp Lys Gly Pro Lys Thr Gly Ser
 805 810 815
 Val Lys Lys Glu Lys Ala Val Lys Pro Glu Glu Gly Gln Leu Val Gln
 820 825 830
 Leu Glu Glu Lys Gly Gln Gly Ser Val Pro Trp Ser Val Tyr Gly Val
 835 840 845
 Tyr Ile Gln Ala Ala Gly Gly Pro Leu Ala Phe Leu Val Ile Met Ala
 850 855 860
 Leu Phe Met Leu Asn Val Gly Ser Thr Ala Phe Ser Thr Trp Trp Leu
 865 870 875 880
 Ser Tyr Trp Ile Lys Gln Gly Ser Gly Asn Thr Thr Val Thr Arg Gly
 885 890 895
 Asn Glu Thr Ser Val Ser Asp Ser Met Lys Asp Asn Pro His Met Gln
 900 905 910
 Tyr Tyr Ala Ser Ile Tyr Ala Leu Ser Met Ala Val Met Leu Ile Leu
 915 920 925
 Lys Ala Ile Arg Gly Val Val Phe Val Lys Gly Thr Leu Arg Ala Ser
 930 935 940
 Ser Arg Leu His Asp Glu Leu Phe Arg Arg Ile Leu Arg Ser Pro Met
 945 950 955 960
 Lys Phe Phe Asp Thr Thr Pro Thr Gly Arg Ile Leu Asn Arg Phe Ser
 965 970 975
 Lys Asp Met Asp Glu Val Asp Val Arg Leu Pro Phe Gln Ala Glu Met
 980 985 990
 Phe Ile Gln Asn Val Ile Leu Val Phe Phe Cys Val Gly Met Ile Ala
 995 1000 1005
 Gly Val Phe Pro Trp Phe Leu Val Ala Val Gly Pro Leu Val Ile Leu
 1010 1015 1020
 Phe Ser Val Leu His Ile Val Ser Arg Val Leu Ile Arg Glu Leu Lys
 1025 1030 1035 1040
 Arg Leu Asp Asn Ile Thr Gln Ser Pro Phe Leu Ser His Ile Thr Ser
 1045 1050 1055
 Ser Ile Gln Gly Leu Ala Thr Ile His Ala Tyr Asn Lys Gly Gln Glu
 1060 1065 1070
 Phe Leu His Arg Tyr Gln Glu Leu Leu Asp Asp Asn Gln Ala Pro Phe
 1075 1080 1085

Phe Leu Phe Thr Cys Ala Met Arg Trp Leu Ala Val Arg Leu Asp Leu
 1090 1095 1100
 Ile Ser Ile Ala Leu Ile Thr Thr Thr Gly Leu Met Ile Val Leu Met
 1105 1110 1115 1120
 His Gly Gln Ile Pro Pro Ala Tyr Ala Gly Leu Ala Ile Ser Tyr Ala
 1125 1130 1135
 Val Gln Leu Thr Gly Leu Phe Gln Phe Thr Val Arg Leu Ala Ser Glu
 1140 1145 1150
 Thr Glu Ala Arg Phe Thr Ser Val Glu Arg Ile Asn His Tyr Ile Lys
 1155 1160 1165
 Thr Leu Ser Leu Glu Ala Pro Ala Arg Ile Lys Asn Lys Ala Pro Ser
 1170 1175 1180
 Pro Asp Trp Pro Gln Glu Gly Glu Val Thr Phe Glu Asn Ala Glu Met
 1185 1190 1195 1200
 Arg Tyr Arg Glu Asn Leu Pro Leu Val Leu Lys Lys Val Ser Phe Thr
 1205 1210 1215
 Ile Lys Pro Lys Glu Lys Ile Gly Ile Val Gly Arg Thr Gly Ser Gly
 1220 1225 1230
 Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val Glu Leu Ser Gly
 1235 1240 1245
 Gly Cys Ile Lys Ile Asp Gly Val Arg Ile Ser Asp Ile Gly Leu Ala
 1250 1255 1260
 Asp Leu Arg Ser Lys Leu Ser Ile Ile Pro Gln Glu Pro Val Leu Phe
 1265 1270 1275 1280
 Ser Gly Thr Val Arg Ser Asn Leu Asp Pro Glu Asn Gln Tyr Thr Glu
 1285 1290 1295
 Asp Gln Ile Trp Asp Ala Leu Glu Arg Thr His Met Lys Glu Cys Ile
 1300 1305 1310
 Ala Gln Leu Pro Leu Lys Leu Glu Ser Glu Val Met Glu Asn Gly Asp
 1315 1320 1325
 Asn Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Ile Ala Arg Ala Leu
 1330 1335 1340
 Leu Arg His Cys Lys Ile Leu Ile Leu Asp Glu Ala Thr Ala Ala Met
 1345 1350 1355 1360
 Asp Thr Glu Thr Asp Leu Leu Ile Gln Glu Thr Ile Arg Glu Ala Phe
 1365 1370 1375
 Ala Asp Cys Thr Met Leu Thr Ile Ala His Arg Leu His Thr Val Leu
 1380 1385 1390

Gly Ser Asp Arg Ile Met Val Leu Ala Gln Gly Gln Val Val Glu Phe
 1395 1400 1405

Asp Thr Pro Ser Val Leu Leu Ser Asn Asp Ser Ser Arg Phe Tyr Ala
 1410 1415 1420

Met Phe Ala Ala Ala Glu Asn Lys Val Ala Val Lys Gly
 1425 1430 1435

<210> 49

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 49

ggtgacagac aagcgagttc agacaatg

28

<210> 50

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 50

ctttgctcct ctgggccagt g

21 ,

<210> 51

<211> 20

<212> DNA

<213> Homo sapiens

<400> 51

ttgtctgcag gtttagcacc

20

<210> 52

<211> 20

<212> DNA

<213> Homo sapiens

<400> 52

ttcatcacag atttcgagtc

20

<210> 53

<211> 20

<212> DNA

<213> Homo sapiens

<400> 53
ttacagacag ttctcattca 20

<210> 54
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<212> DNA
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<400> 54
ttctttccag gtgctcaata 20

<210> 55
<211> 20
<212> DNA
<213> Homo sapiens

<400> 55
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<210> 56
<211> 20
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<213> Homo sapiens

<400> 56
tattttgcag atataagaag 20

<210> 57
<211> 20
<212> DNA
<213> Homo sapiens

<400> 57
tgttcttcag gcatttagtg 20

<210> 58
<211> 20
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<213> Homo sapiens

<400> 58
ttaatcttag aaaattctca 20

<210> 59
<211> 20
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<400> 59
tctctggcag gggaagatct 20

<210> 60
 <211> 20
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<400> 60
 gttgttccag atgcagctgc 20

<210> 61
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 61
 gcaccaacag gtatcagcac 20

<210> 62
 <211> 20
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 <213> Homo sapiens

<400> 62
 ctgtccacag attggggagc 20

<210> 63
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 63
 acttctgcag ttcttagagt 20

<210> 64
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